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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=2; day=12; hr=10; min=20; sec=51; ms=504; ]

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Application No: 10521518

Version No: 3.0

Input Set:

Output Set:

Started: 2009-01-26 15:40:47.658

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Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 888 ms

Total Warnings: 0

Total Errors: 8

No. of SeqIDs Defined: 110

Actual SeqID Count: 110

Error code	Error Description
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E 320	Wrong Nucleic Acid Designator, at in SEQID (9)
E 320	Wrong Nucleic Acid Designator, aa in SEQID (11)
E 320	Wrong Nucleic Acid Designator, aa in SEQID (13)
E 320	Wrong Nucleic Acid Designator, ag in SEQID (17)
E 320	Wrong Nucleic Acid Designator, at in SEQID (19)
E 320	Wrong Nucleic Acid Designator, at in SEQID (25)
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<110> Expressive Research B.V.

<120> Modulating developmental pathways in plants

<130> 294-208 PCT/US

<140> 10521518

<141> 2006-02-28

<150> PCT/NL03/00524

<151> 2003-07-17

<150> EP 02077908.8

<151> 2002-07-17

<160> 110

<170> PatentIn version 3.2

<210> 1

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<212> PRT

<213> Arabidopsis thaliana

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Cys Gly Cys Cys Leu Leu Ser Leu Phe Val Lys Val Ile Ile Ser Leu  
35 40 45

Ile Val Ile Leu Gly Val Ala Ala Leu Ile Phe Trp Leu Ile Val Arg  
50 55 60

Pro Arg Ala Ile Lys Phe His Val Thr Asp Ala Ser Leu Thr Arg Phe  
65 70 75 80

Asp His Thr Ser Pro Asp Asn Ile Leu Arg Tyr Asn Leu Ala Leu Thr  
85 90 95

Val Pro Val Arg Asn Pro Asn Lys Arg Ile Gly Leu Tyr Tyr Asp Arg  
100 105 110

Ile Glu Ala His Ala Tyr Tyr Glu Gly Lys Arg Phe Ser Thr Ile Thr  
115 120 125

Leu Thr Pro Phe Tyr Gln Gly His Lys Asn Thr Thr Val Leu Thr Pro  
130 135 140

Thr Phe Gln Gly Gln Asn Leu Val Ile Phe Asn Ala Gly Gln Ser Arg  
145 150 155 160

Thr Leu Asn Ala Glu Arg Ile Ser Gly Val Tyr Asn Ile Glu Ile Lys  
165 170 175

Phe Arg Leu Arg Val Arg Phe Lys Leu Gly Asp Leu Lys Phe Arg Arg  
180 185 190

Ile Lys Pro Lys Val Asp Cys Asp Asp Leu Arg Leu Pro Leu Ser Thr  
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Leu Asn Leu Ser Ile Arg Asn Ser Lys Ser Ser Ile Gly Ile His Tyr  
35 40 45

Asp Arg Phe Glu Ala Thr Val Tyr Tyr Met Asn Gln Arg Leu Gly Ala  
50 55 60

Val Pro Met Pro Leu Phe Tyr Leu Gly Ser Lys Asn Thr Met Leu Leu  
65 70 75 80

Arg Ala Leu Phe Glu Gly Gln Thr Leu Val Leu Leu Lys Gly Asn Glu  
85 90 95

Arg Lys Lys Phe Glu Asp Asp Gln Lys Thr Gly Val Tyr Arg Ile Asp  
100 105 110

Val Lys Leu Ser Ile Asn Phe Arg Val Met Val Leu His Leu Val Thr  
115 120 125

Trp Pro Met Lys Pro Val Val Arg Cys His Leu Lys Ile Pro Leu Ala  
130 135 140

Leu Gly Ser Ser Asn Ser Thr Gly Gly His Lys Lys Met Leu Leu Ile  
145 150 155 160

Gly Gln Leu Val Lys Asp Thr Ser Ala Asn Leu Arg Glu Ala Ser Glu  
165 170 175

Thr Asp His Arg Arg Asp Val Ala Gln Ser Lys Lys Ile Ala Asp Ala  
180 185 190

Lys Leu Ala Lys Asp Phe Glu Ala Ala Leu Lys Glu Phe Gln Lys Ala  
195 200 205

Gln His Ile Thr Val Glu Arg Glu Thr Ser Tyr Ile Pro Phe Asp Pro  
210 215 220

Lys Gly Ser Phe Ser Ser Ser Glu Val Asp Ile Gly Tyr Asp Arg Ser  
225 230 235 240

Gln Glu Gln Arg Val Leu Met Glu Ser Arg Arg Gln Glu Ile Val Leu  
245 250 255

Leu Asp Asn Glu Ile Ser Leu Asn Glu Ala Arg Ile Glu Ala Arg Glu  
260 265 270

Gln Gly Ile Gln Glu Val Lys His Gln Ile Ser Glu Val Met Glu Met  
275 280 285

Phe Lys Asp Leu Ala Val Met Val Asp His Gln Gly Thr Ile Asp Asp  
290 295 300

Ile Asp Glu Lys Ile Asp Asn Leu Arg Ser Ala Ala Ala Gln Gly Lys  
 305 310 315 320

Ser His Leu Val Lys Ala Ser Asn Thr Gln Gly Ser Asn Ser Ser Leu  
 325 330 335

Leu Phe Ser Cys Ser Leu Leu Leu Phe Phe Phe Leu Ser Gly Asp Leu  
 340 345 350

Cys Arg Cys Val Cys Val Gly Ser Glu Asn Pro Arg Leu Asn Pro Thr  
 355 360 365

Arg Arg Lys Ala Trp Cys Glu Glu Glu Asp Glu Glu Gln Arg Lys Lys  
 370 375 380

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agttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcatc	240
ctccgaaaaa agggaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca	300
aatgcaatct ataatctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag	360
cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa	420
gtagctgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc	480
aaaatcacta ctcaagaaat atg aag aag atg aat gtg gtg gct ttt gtt acg	533
Met Lys Lys Met Asn Val Val Ala Phe Val Thr	
1 5 10	
ctg atc atc tct ttt ctt ctg ctt tct cag gttaaactgtt aaaaccattt	583
Leu Ile Ile Ser Phe Leu Leu Leu Ser Gln	
15 20	
tcaagactac cttttctcta tttcagacaa accaaagtaa aacaatgaaa aatctctctg	643
gtctttcata g gta ctt gca gag ttg tca tca tcc agc aac aat gaa act	693
Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn Glu Thr	
25 30	
tcc tct gtt tct cag gtaagagtga tacaaaaaca tactaaacaa actttcaaga	748
Ser Ser Val Ser Gln	
35	
gagtaatata taaggaaatg ttggcttctt ttttttggtg ctaatcag acg aat gac	805
Thr Asn Asp	
40	
gag aac caa act gcg gcg ttt aag aga aca tac cac cat cgt cca aga	853
Glu Asn Gln Thr Ala Ala Phe Lys Arg Thr Tyr His His Arg Pro Arg	
45 50 55	
atc agttagteta ctctttcaac actctaattc ctttggttcta agtatTTTTT	906
Ile	
ttgcccccca caaccttttt tttattaaat gagccaattt ttatagat tgt ggg cat	963
Cys Gly His	
60	
gca tgc gca agg aga tgc agt aag aca tcg agg aag aaa gtt tgt cac	1011
Ala Cys Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His	
65 70 75	
aga gcc tgt gga agt tgt tgt gcc aag tgt cag tgt gtg ccg ccg gga	1059
Arg Ala Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly	
80 85 90	

acc tcc ggc aac aca gca tca tgt cct tgc tac gcc agt atc cgt aca 1107  
Thr Ser Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr  
95 100 105 110

cat ggc aat aaa ctc aaa tgt cct taaaagactt ctcatttctc aactatagtc 1161  
His Gly Asn Lys Leu Lys Cys Pro  
115

tcaccttctg attatgtttc ttcttttgtt atgttgcatg tgtgatgtgt gagcttatta 1221

ttatgttgat tgttgacata attcaactat ataatttgta tcgattccga ataataagat 1281

gagtgatttt attggctatt aagttttttt tttttttttt tgggcacaat ggctattaag 1341

ttttaaacat ctgattttat tggttacaaa aaacaacaaa gtttcatttt catattaaca 1401

caaaatctcc atacatatta ccaaaccaaa aaaatacaca agggggagag agaccaacgg 1461

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Glu Thr Ser Ser Val Ser Gln Thr Asn Asp Glu Asn Gln Thr Ala Ala  
35 40 45

Phe Lys Arg Thr Tyr His His Arg Pro Arg Ile Cys Gly His Ala Cys  
50 55 60

Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His Arg Ala  
65 70 75 80

Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly Thr Ser  
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Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr His Gly



Asn Lys Leu Lys Cys Pro  
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tttgtgttta tgtttgattt tacgttttta tatgtaaata agatatttta cgaattatgg 180  
  
ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat 240  
  
aaagtaatat aatatatgta ccgttattaa cttattgtac atgtgaatga ggaagcttac 300  
  
acacacacac cttctataaa tagctgacaa aactggttgt tacacacaac acattcataa 360  
  
atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc 420  
  
tctctcaaga gctagtcatt gccaaactca taacttcttt tctcttactc acaattttat 480  
  
tcactttcgt ttgtctcact atg tca aaa gaa gct gag tac cat cca gaa agt 533  
Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser  
1 5 10  
  
gtaagttttt attttttggt aaaatagaaa gtgtaagttt tataattcat tcaattgttt 593  
  
ttgcctttcc ctttctattt attgctataa atctaatacc cgcgttaaaa ttggttttga 653  
  
aattaaacag tat gga cca gga agt ctg aaa tca tac c gtaagtaaaa 701  
Tyr Gly Pro Gly Ser Leu Lys Ser Tyr  
15 20

acttcttctt cttttatgaa tcttgtttct tattatatat caaataaaaa ctcgattatc 761

atgattgcag aa tgt gga gga caa tgc aca agg aga tgt agc aac aca 809  
Gln Cys Gly Gly Gln Cys Thr Arg Arg Cys Ser Asn Thr  
25 30

aag tat cat aag cca tgc atg ttc ttc tgc caa aag tgt tgt gct aaa 857  
Lys Tyr His Lys Pro Cys Met Phe Phe Cys Gln Lys Cys Cys Ala Lys  
35 40 45

tgc ctt tgt gtc cct cca ggc acg tac ggc aac aaa caa gtg tgt cct 905  
Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro  
50 55 60 65

tgt tac aac aac tgg aag act caa caa ggt gga cca aaa tgt cca 950  
Cys Tyr Asn Asn Trp Lys Thr Gln Gln Gly Gly Pro Lys Cys Pro  
70 75 80

taaacaaaaa cattgagaga gaaaccccaa tctgtttcct attttattta attatttcca 1010

gtatgctttt gttgtcgtga tggttaaatt atagtgtttt tgcagggtatc atttatcatc 1070

gataaacaat atcatataaa atcttctatg tttctttcac gttttgtttc ttttgttgta 1130

gtcaatacac gaaatgtgta tggaccttct aattaggaat atataaaaatt ttatttatta 1190

attagataat ctttcgtata gttaaaattc caaggattac ttttgattcg tttgggacaa 1250

tctattttat attttacttt ctaagtttgt ataactatat cttaaaagtg ttagacagag 1310

tcctaatagat tttagtataa ttgttactat ttagttacgc ttcgaaaatt tggaactttt 1370

ccaaagtggc ctatatcaat ttgattcact aatctgcgct tccttctagt tttttacaat 1430

tatggagatt tttcgacgat gat 1453

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<213> Arabidopsis thaliana

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Thr Lys Tyr His Lys Pro Cys Met Phe Phe Cys Gln Lys Cys Cys Ala  
35 40 45

Lys Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly Asn Lys Gln Val Cys

Pro Cys Tyr Asn Asn Trp Lys Thr Gln Gln Gly Gly Pro Lys Cys Pro  
 65 70 75 80

<210> 7  
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 atcaatatct attgcaaaaa atatttataa gaatacaaat gaaaaatgat aaaatacaaa 180  
 tgattttctca attacctaaa aaatataaaa atgtcttact ttatttttcag ccactgttgg 240  
 aaagtacttg caatcatatc gtatttttgaa ttataaaact cagaaacaat tattttccct 300  
 gaaaagttaa aactttttaat aagatattta taaaataaaa agaatagtct agaccgaaaa 360  
 tggggtcggt tgtccatcca aaggagtgc ataaatagaa cctccaagt tctcattagg 420  
 acacaacaac taaaaccaca tttatcatta cagtctgatt tgagctaagt tctctcatca 480  
 taaactctcc ttggagaatc atg gct att tca aaa gct ctt atc gct tct ctt 533  
 Met Ala Ile Ser Lys Ala Leu Ile Ala Ser Leu  
 1 5 10  
 ctc ata tct ctt ctt gtt ctc caa ctc gtc cag gctgatgtcg tacgtctttt 586  
 Leu Ile Ser Leu Leu Val Leu Gln Leu Val Gln  
 15 20  
 tcatcacaaa ctaattatac tcaatataat acttatgttt tcaaaaacat atttctcaca 646  
 tgttacaaca atattcttgc ag gaa aac tca cag aag aaa aat ggt tac gca 698  
 Glu Asn Ser Gln Lys Lys Asn Gly Tyr Ala

aag aag atc g gtaattatat gattttttatt aaacctaacg ttaaatttag 748

Lys Lys Ile

35

agtgagatta ataatctgtg tttttctttc ttgtatatat ag at tgt ggg agt 801

Asp Cys Gly Ser

gcg tgt gta gca cgg tgc agg ctt tcg agg agg ccg agg ctg tgt cac 849

Ala Cys Val Ala Arg Cys Arg Leu Ser Arg Arg Pro Arg Leu Cys His

40

45

50

55

aga gcg tgc ggg act tgc tgc tac agg tgc aac tgt gtg cct ccg ggt 897